

2902076-1_ST25.txt
SEQUENCE LISTING

<110> The University of York

<120> Expansion Polypeptides

<130> 2902076.1

<140> 10/573,245

<141> 2006-03-23

<150> PCT/GB04/04058

<151> 2004-09-23

<160> 24

<170> PatentIn version 3.4

<210> 1

<211> 783

<212> DNA

<213> Craterostigma plantagineum

<220>

<221> CDS

<222> (1)..(783)

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1				5					10				15			

acc	agc	agc	agc	cat	ttt	gcg	cgc	gcg	tat	tat	ggc	ggc	gat	ggc	ggc	96
Thr	Ser	Ser	Ser	His	Phe	Ala	Arg	Ala	Tyr	Tyr	Gly	Gly	Asp	Gly	Gly	
			20					25					30			

tgg	acc	gat	gcg	cat	gcg	acc	ttt	tat	ggc	ggc	agc	gat	gcg	agc	ggc	144
Trp	Thr	Asp	Ala	His	Ala	Thr	Phe	Tyr	Gly	Gly	Ser	Asp	Ala	Ser	Gly	
		35					40					45				

acc	atg	ggc	ggc	gcg	tgc	ggc	tat	ggc	aac	ctg	tat	agc	cag	ggc	tat	192
Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	
	50				55					60						

ggc	acc	aac	acc	gcg	gcg	ctg	agc	acc	gcg	ctg	ttt	aac	aac	ggc	ctg	240
Gly	Thr	Asn	Thr	Ala	Ala	Leu	Ser	Thr	Ala	Leu	Phe	Asn	Asn	Gly	Leu	
65				70					75					80		

agc	tgc	ggc	agc	tgc	ttt	gaa	att	aaa	tgc	gcg	agc	agc	att	agc	ggc	288
Ser	Cys	Gly	Ser	Cys	Phe	Glu	Ile	Lys	Cys	Ala	Ser	Ser	Ile	Ser	Gly	
			85						90					95		

ggc	ggc	aaa	tgg	tgc	ctg	ccg	ggc	ggc	agc	att	acc	gtg	acc	gcg	acc	336
Gly	Gly	Lys	Trp	Cys	Leu	Pro	Gly	Gly	Ser	Ile	Thr	Val	Thr	Ala	Thr	
			100				105						110			

aac	ttt	tgc	ccg	ccg	aac	aac	gcg	ctg	ccg	aac	aac	gcg	ggc	ggc	tgg	384
Asn	Phe	Cys	Pro	Pro	Asn	Asn	Ala	Leu	Pro	Asn	Asn	Ala	Gly	Gly	Trp	
		115					120					125				

tgc	aac	ccg	ccg	ctg	cag	cat	ttt	gat	ctg	agc	cag	ccg	gtg	ttt	cag	432
Cys	Asn	Pro	Pro	Leu	Gln	His	Phe	Asp	Leu	Ser	Gln	Pro	Val	Phe	Gln	

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140

130

135

cat att gcg cag tat cgc gcg ggc att gtg ccg gtg agc tat cgc cgc 480
His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg
145 150 155 160

gtg ccg tgc cgc cgc cgc ggc ggc att cgc ttt acc att aac ggc cat 528
Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His
165 170 175

agc tat ttt aac ctg gtg ctg att acc aac gtg ggc ggc gcg ggc gat 576
Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp
180 185 190

gtg cat gcg gtg agc att aaa ggc gcg acc acc gat tgg cag ccg atg 624
Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met
195 200 205

agc cgc aac tgg ggc cag aac tgg cag agc aac gcg aac ccg aac ggc 672
Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly
210 215 220

cag cgc ctg agc ttt aaa gtg acc acc agc gat ggc cgc acc ctg gtg 720
Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val
225 230 235 240

agc aac aac gtg gcg ccg ccg aac tgg agc ttt ggc cag acc ttt gcg 768
Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala
245 250 255

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Gly Ala Gln Phe Asn
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<213> Craterostigma plantagineum

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Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
35 40 45

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr
50 55 60

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
65 70 75 80

Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
Page 2

Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr
100 105 110

Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp
115 120 125

Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln
130 135 140

His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg
145 150 155 160

Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His
165 170 175

Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp
180 185 190

Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met
195 200 205

Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly
210 215 220

Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val
225 230 235 240

Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala
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Gly Ala Gln Phe Asn
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<222> (1)..(657)

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Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala
1 5 10 15

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tgc ggc tat ggc aac ctg tat agc acc ggc tat ggc acc aac acc gcg
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Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Thr	Gly	Tyr	Gly	Thr	Asn	Thr	Ala		
			20					25					30				
gcg	ctg	agc	acc	gcg	ctg	ttt	aac	aac	ggc	ctg	acc	tgc	ggc	gcg	tgc		144
Ala	Leu	Ser	Thr	Ala	Leu	Phe	Asn	Asn	Gly	Leu	Thr	Cys	Gly	Ala	Cys		
		35					40					45					
tat	gaa	ctg	acc	tgc	aac	aac	gat	ccg	cgc	ggc	tgg	tgc	ctg	agc	ggc		192
Tyr	Glu	Leu	Thr	Cys	Asn	Asn	Asp	Pro	Arg	Gly	Trp	Cys	Leu	Ser	Gly		
	50					55					60						
acc	att	atg	gtg	acc	gcg	acc	aac	ttt	tgc	ccg	ccg	aac	ccg	agc	ctg		240
Thr	Ile	Met	Val	Thr	Ala	Thr	Asn	Phe	Cys	Pro	Pro	Asn	Pro	Ser	Leu		
65					70				75						80		
ccg	aac	gat	aac	ggc	ggc	tgg	tgc	aac	ccg	ccg	cgc	cag	cat	ttt	gat		288
Pro	Asn	Asp	Asn	Gly	Gly	Trp	Cys	Asn	Pro	Pro	Arg	Gln	His	Phe	Asp		
				85					90					95			
ctg	gcg	gaa	ccg	gcg	ttt	ctg	cag	att	gcg	cag	tat	aaa	gcg	ggc	att		336
Leu	Ala	Glu	Pro	Ala	Phe	Leu	Gln	Ile	Ala	Gln	Tyr	Lys	Ala	Gly	Ile		
			100					105					110				
gtg	ccg	gtg	aac	tat	cgc	cgc	gtg	ccg	tgc	cag	aaa	aaa	ggc	ggc	att		384
Val	Pro	Val	Asn	Tyr	Arg	Arg	Val	Pro	Cys	Gln	Lys	Lys	Gly	Gly	Ile		
		115					120					125					
cgc	ttt	acc	att	aac	ggc	cat	agc	ttt	ttt	aac	ctg	gtg	ctg	gtg	acc		432
Arg	Phe	Thr	Ile	Asn	Gly	His	Ser	Phe	Phe	Asn	Leu	Val	Leu	Val	Thr		
	130					135					140						
aac	gtg	ggc	ggc	gtg	ggc	gat	gtg	cat	agc	gtg	agc	att	aaa	ggc	agc		480
Asn	Val	Gly	Gly	Val	Gly	Asp	Val	His	Ser	Val	Ser	Ile	Lys	Gly	Ser		
145					150					155					160		
aac	ggc	ggc	tgg	cag	ccg	ctg	agc	cgc	aac	tgg	ggc	cag	aac	tgg	cag		528
Asn	Gly	Gly	Trp	Gln	Pro	Leu	Ser	Arg	Asn	Trp	Gly	Gln	Asn	Trp	Gln		
				165					170					175			
agc	aac	agc	tat	ctg	aac	ggc	cag	agc	ctg	agc	ttt	cag	gtg	acc	acc		576
Ser	Asn	Ser	Tyr	Leu	Asn	Gly	Gln	Ser	Leu	Ser	Phe	Gln	Val	Thr	Thr		
			180					185					190				
agc	gat	ggc	cgc	acc	gtg	acc	agc	tat	gat	gtg	gcg	ccg	cgc	ggc	tgg		624
Ser	Asp	Gly	Arg	Thr	Val	Thr	Ser	Tyr	Asp	Val	Ala	Pro	Arg	Gly	Trp		
		195					200					205					
cag	ttt	ggc	cag	acc	ttt	gaa	ggc	ggc	cag	ttt							657
Gln	Phe	Gly	Gln	Thr	Phe	Glu	Gly	Gly	Gln	Phe							
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Ala	Thr	Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala	
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Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala
20 25 30

Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys
35 40 45

Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly
50 55 60

Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu
65 70 75 80

Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp
85 90 95

Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile
100 105 110

Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile
115 120 125

Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr
130 135 140

Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser
145 150 155 160

Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln
165 170 175

Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr
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Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp
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Gln Phe Gly Gln Thr Phe Glu Gly Gly Gln Phe
210 215

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<222> (1)..(672)

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2902076-1_ST25.txt

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ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat ggc acc aac Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn 20 25 30	96
acc gcg gcg ctg agc acc acc ctg ttt aac aac ggc ctg gcg tgc ggc Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly 35 40 45	144
agc tgc tat cag gtg cgc tgc gaa ggc ggc ccg aaa tgg tgc gtg cgc Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg 50 55 60	192
ggc ggc gat cgc att att acc gtg acc gcg acc aac ttt tgc ccg ccg Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro 65 70 75 80	240
aac tat gcg ctg gcg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg 85 90 95	288
cag cat ttt gat atg gcg cag ccg gcg ttt gtg cgc att gcg cat tat Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr 100 105 110	336
cgc gcg ggc att gtg ccg att agc tat cgc cgc gtg agc tgc gtg aaa Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys 115 120 125	384
aaa ggc ggc att cgc ctg acc att aac ggc cat agc tat ttt aac ctg Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu 130 135 140	432
gtg ctg gtg agc aac gtg ggc ggc agc ggc gat gtg cat gcg gtg tgg Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp 145 150 155 160	480
att aaa ggc agc ggc ggc ggc ccg tgg cag gcg atg acc cgc aac tgg Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp 165 170 175	528
ggc cag aac tgg cag agc aac agc tat ctg gat ggc cag agc ctg agc Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser 180 185 190	576
ttt att gtg cgc gcg ggc gat ggc cgc acc gtg acc gcg aac gab att Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile 195 200 205	624
gtg ccg cgc ggc tgg cag ttt ggc cag acc ttt gaa ggc ccg cag ttt Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe 210 215 220	672

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<223> The 'Xaa' at location 207 stands for Glu, or Asp.

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Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn
 20 25 30

Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly
 35 40 45

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg
 50 55 60

Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro
 65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg
 85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr
 100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys
 115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu
 130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp
 145 150 155 160

Ile Lys Gly Ser Gly Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp
 165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser
 180 185 190

Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile
 195 200 205

Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe
 210 215 220

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 <222> (3)..(3)
 <223> n is a, c, g, or t

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 <222> (6)..(6)
 <223> y is pyrimidine

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 <223> n is a, c, g, or t

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 <223> y is pyrimidine

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 <222> (10)..(10)
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 <223> n is a, c, g, or t

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 aagcagtggg atcaacgcag agt 23

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 gctcagtata cagctgggat tgtg 24

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